## AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Please delete the sentence at page 3, lines 10–11, as amended in the Reply After 1st Office Action Under 37 CFR §1.111(b), and insert the following sentence:

Figures 7-102 show the atomic structure coordinates for HPTPbeta as derived from a monoclinic crystal of ligand-free HPTPbeta catalytic domain [SEQ ID NO: 7] polypeptide.

Please delete the sentence at page 3, lines 14–15, as amended in the Reply After 1st Office Action Under 37 CFR §1.111(b), and insert the following sentence:

Figures 202-252 show the atomic structure coordinates for HPTPbeta as derived from a orthorhombic crystal of ligand-free HPTPbeta catalytic domain [SEQ ID NO: 7] polypeptide.

## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1–9 (Canceled).

10. (New) A computer-implemented method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:

(a) providing X, Y and Z atomic structure coordinates set forth in any of Figures 7-304 for all or a portion of a crystalline form of an HPTPbeta catalytic domain;

(b) determining a three-dimensional structure of all or a portion of a crystalline form of an HPTPbeta catalytic domain from said X, Y and Z coordinates;

(c) imaging said three-dimensional structure of all or a portion of a crystalline form of an HPTPbeta catalytic domain;

(d) positioning one or more candidate compounds at one or more areas of said imaged three-dimensional structure by using binding mode(s) of said one or more candidate compounds with said area(s) of said imaged three-dimensional structure; and

(e) identifying from said one or more candidate compounds those that bind or modulate HPTPbeta as drug candidate compounds useful for the treatment of an angiogenesis mediated disorder.

11. (New) The method of claim 10, further comprising determining the one or more locations or binding geometries of said positioned one or more candidate compounds relative to any of said X, Y and Z atomic structure coordinates.

12. (New) The method of claim 10, further comprising assembling fragments of said one or more candidate compounds together to create an assembled compound.

13. (New) The method of claim 12, further comprising analyzing the ability of said assembled compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

14. (New) The method of claim 10, wherein said one or more candidate compounds or portion(s) thereof are HPTPbeta agonists.

15. (New) The method of claim 14, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

16. (New) The method of claim 10, wherein said one or more candidate compounds or portion(s) therof are HPTPbeta antagonists.

17. (New) The method of claim 16, further comprising analyzing the ability of said one or more candidate compounds to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

18. (New) The method of claim 10, wherein said X, Y and Z atomic structure coordinates of said three-dimensional structure are HPTPbeta binding sites or combinations thereof.

19. (New) The method of claim 10, wherein said one or more candidate compounds are positioned at at least one of the P(0), P(+1) and P(-1) binding sites of HPTPbeta.

20. (New) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290 and 293 of SEQ ID NO: 7.

21. (New) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.

22. (New) The method of claim 18, wherein said one or more candidate compounds are positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.

23. (New) The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain has unit cell dimensions of approximately a=39 Å, b=71Å, c=120 Å, $\alpha$=90°, $\beta$=90°, $\gamma$=90° in the space group $P2_12_12_1$.

24. (New) The method of claim 10, wherein said crystalline form of an HPTPbeta catalytic domain has unit cell dimensions of approximately a=62 Å, b=72Å, c=70 Å, $\alpha$=90°, $\beta$=93°, $\gamma$=90° in the space group $P2_1$.

25. (New) A method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:

(a) imaging, through the use of computer modeling of X, Y and Z atomic structure coordinates set forth in Figures 202-252, a crystalline form of an HPTPbeta catalytic domain using unit cell dimensions of approximately a=39 Å, b=71Å, c=120 Å, $\alpha$=90°, $\beta$=90°, $\gamma$=90° in the space group $P2_12_12_1$;

(b) computationally positioning a drug candidate compound at one or more areas of said imaged HPTPbeta catalytic domain by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain; and

(c) analyzing the ability of said drug candidate compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

26. (New) A method of identifying a drug candidate compound for the treatment of an angiogenesis mediated disorder, comprising:

(a) imaging, through the use of computer modeling of X, Y and Z atomic structure coordinates set forth in Figures 7-102, a crystalline form of an HPTPbeta catalytic domain using unit cell dimensions of approximately a=62 Å, b=72 Å, c=70 Å, $\alpha$=90°, $\beta$=93°, $\gamma$=90° in the space group $P2_1$;

(b) computationally positioning a drug candidate compound at one or more areas of said imaged HPTPbeta catalytic domain by using a binding mode of said drug candidate compound with said area(s) of said imaged HPTPbeta catalytic domain; and

(c) analyzing the ability of said drug candidate compound to bind or modulate HPTPbeta in an *in vivo* or *in vitro* assay.

27. (New) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290 and 293 of SEQ ID NO: 7.

28. (New) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 152, 74-77, 209-214, 244-253, 288-290 and 293 of SEQ ID NO: 7.

29. (New) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.

30. (New) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 76-80, 48-66, 284-292 and 212-214 of SEQ ID NO: 7.

31. (New) The method according to claim 25, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.

32. (New) The method according to claim 26, wherein said drug candidate compound is positioned at at least amino acid residues 69-76, 119-123 and 149-154 of SEQ ID NO: 7.